RAW SEQUENCE LISTING   DATE: 01/12/2001
PATENT APPLICATION: US/09/218,913A   TIME: 10:23:22

Input Set : A:\Pto.amc
Output Set: N:\CRF3\01112001\I218913A.raw

```
212 Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met
213         35              40              45
215 Leu Arg Cys
216      50
218 <210> SEQ ID NO: 8
219 <211> LENGTH: 92
220 <212> TYPE: PRT
221 <213> ORGANISM: Homo sapien
223 <400> SEQUENCE: 8
224 Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val
225 1               5               10              15
227 Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr
228         20              25              30
230 Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser
231         35              40              45
233 Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val
234      50              55              60
236 Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp
237 65              70              75              80
239 Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser
240              85              90
242 <210> SEQ ID NO: 9
243 <211> LENGTH: 708
244 <212> TYPE: DNA
245 <213> ORGANISM: Homo sapien
247 <220> FEATURE:
248 <221> NAME/KEY: misc_feature
249 <222> LOCATION: 679..708
250 <223> OTHER INFORMATION: /note= "n at positions 622, 679, 707 is any nucleic acid"
252 <400> SEQUENCE: 9
253 ggccgggtcg tttctcgcct ggctgggatc gctgctcctc tctggggtcc tggcggccga      60
255 ccgagaacgc agcatccacg acttctgcct ggtgtcgaag gtggtgggca gatgccgggc     120
257 ctccatgcct aggtggtggt acaatgtcac tgacggatcc tgccagctgt ttgtgtatgg     180
259 gggctgtgac ggaaacagca ataattacct gaccaaggag gagtgcctca agaaatgtgc     240
261 cactgtcaca gagaatgcca cgggtgacct ggccaccagc aggaatgcag cggattcctc     300
263 tgtcccaagt gctcccagaa ggcaggattc tgaagaccac tccagcgata tgttcaacta     360
265 tgaagaatac tgcaccgcca acgcagtcac tgggccttgc cgtgcatcct tcccacgctg     420
267 gtactttgac gtggagagga actcctgcaa taacttcatc tatggaggct gccggggcaa     480
269 taagaacagc taccgctctg aggaggcctg catgctccgc tgcttccgcc agcaggagaa     540
271 tcctcccctg ccccttggct caaaggtggt ggttctggcc ggggctgttt cgtgatggtg     600
273 ttgatccttt tcctggggag cntccatggt cttactgatt ccgggtggca aggaggaacc     660
275 aggagcgtgc cctgcgggan cgtctggagct tcggagatga caagggnt                 708
277 <210> SEQ ID NO: 10
278 <211> LENGTH: 235
279 <212> TYPE: PRT
280 <213> ORGANISM: Homo sapien
282 <220> FEATURE:
283 <221> NAME/KEY: peptide
284 <222> LOCATION: 1..235
```

see next page

```
                RAW SEQUENCE LISTING          DATE: 01/12/2001
                PATENT APPLICATION: US/09/218,913A    TIME: 10:23:22

                Input Set : A:\Pto.amc
                Output Set: N:\CRF3\01112001\I218913A.raw

     285 <223> OTHER INFORMATION: /note= "Xaa at positions 201, 226, and 233 are nonsence or stop codons"
     287 <400> SEQUENCE: 10
     288 Ala Gly Ser Phe Leu Ala Trp Leu Gly Ser Leu Leu Leu Ser Gly Val
     289 1               5                   10                  15
     291 Leu Ala Ala Asp Arg Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser
     292             20                  25                  30
     294 Lys Val Val Gly Arg Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn
     295             35                  40                  45
     297 Val Thr Asp Gly Ser Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly
     298         50                  55                  60
     300 Asn Ser Asn Asn Tyr Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala
     301 65                  70                  75                  80
     303 Thr Val Thr Glu Asn Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala
     304             85                  90                  95
     306 Ala Asp Ser Ser Val Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp
     307             100                 105                 110
     309 His Ser Ser Asp Met Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala
     310         115                 120                 125
     312 Val Thr Gly Pro Cys Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val
     313         130                 135                 140
     315 Glu Arg Asn Ser Cys Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn
     316 145                 150                 155                 160
     318 Lys Asn Ser Tyr Arg Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg
     319             165                 170                 175
     321 Gln Gln Glu Asn Pro Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu
     322             180                 185                 190
W--> 324 Ala Gly Ala Val Ser Xaa Trp Cys Xaa Ser Phe Ser Trp Gly Ala Ser
     325         195                 200                 205
     327 Met Val Leu Leu Ile Pro Gly Gly Lys Glu Glu Pro Gly Ala Cys Pro
     328         210                 215                 220
W--> 330 Ala Xaa Arg Leu Glu Leu Arg Arg Xaa Gln Gly
     331 225                 230                 235
     333 <210> SEQ ID NO: 11
     334 <211> LENGTH: 179
     335 <212> TYPE: PRT
     336 <213> ORGANISM: Homo sapien
     338 <220> FEATURE:
     339 <221> NAME/KEY: peptide
     340 <222> LOCATION: 1..170
     341 <223> OTHER INFORMATION: /note= "Xaa at positions 8, 17, 19, 21-26, 40, 42, 45-47, 52, 64,
     342         103, 112, 114, 116-121, 135, 137, 140-142, 147, and 159 is any
     343         amino acid residue"
     345 <400> SEQUENCE: 11
W--> 346 Ala Asp Arg Glu Arg Ser Ile Xaa Asp Phe Cys Leu Val Ser Lys Val
     347 1               5                   10                  15
  -> 349 Xaa Gly Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Trp Trp Tyr Asn Val Thr
     350             20                  25                  30
  -> 352 Asp Gly Ser Cys Gln Leu Phe Xaa Tyr Xaa Gly Cys Xaa Xaa Xaa Ser
     353         35                  40                  45
```

[Handwritten annotations:]

invalid use of Xaa

(circled: nonsence or stop codons)

Xaa can only represent a single amino acid, nothing else. ✳

what about Xaa at position 198?

✳ FYI, per 1.822(5)(e) of new sequence Rules, "a sequence with a gap or gaps shall be presented as a plurality of separate sequences..."

(circled "OK")

FYI

Please Note:
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.**